



1

SEQUENCE LISTING

<110> SCHLESSINGER, JOSEPH
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FUCHS, MIRIAM

<120> NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA

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<151> 1993-07-01

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Ser Ser Asn His Asp Pro Gly Glu Lys Ala Arg Leu Gln Leu Pro Thr
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Met Lys Glu Asn Asp Thr His Cys Ile Asp Phe Ser Tyr Leu Leu Tyr
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Ser Gln Lys Gly Leu Asn Pro Gly Thr Leu Asn Ile Leu Val Arg Val
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Gln Glu Val Thr Lys Thr Asp Gln Asp Leu Tyr Arg Cys Val Thr Gln
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Pro Ile Ile Leu Lys Glu Val Glu Tyr Arg Met Thr Ser Gly Ser Trp
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Tyr Ser Gln Lys Gly Leu Asn Pro Gly Thr Leu Asn Ile Leu Val Arg
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Trp Gln Glu Glu Trp Lys Glu Gly Glu Gly Arg Thr Ile Ile His Cys
 1365 1370 1375

Leu Asn Gly Gly Arg Ser Gly Met Phe Cys Ala Ile Gly Ile Val
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Val Glu Met Val Lys Arg Gln Asn Val Val Asp Val Phe His Ala Val
 1395 1400 1405

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 Gly Gly Cys Thr Phe Asp Asp Gly Pro Gly Ala Cys Asp Tyr His Gln
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gat tta tac gat gac ttt gag tgg gtc cat gtc agt gcg cag gaa cct 192
 Asp Leu Tyr Asp Asp Phe Glu Trp Val His Val Ser Ala Gln Glu Pro
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cat tac ctg ccc ccc gaa atg cct caa ggt tcc tat atg gtt gtg gac 240
 His Tyr Leu Pro Pro Glu Met Pro Gln Gly Ser Tyr Met Val Val Asp
 65 70 75 80

tcc tca aat cat gat cct gga gaa aaa gcc aga ctt cag ctg cct acc 288
 Ser Ser Asn His Asp Pro Gly Glu Lys Ala Arg Leu Gln Leu Pro Thr
 85 90 95

atg aag gag aat gac acc cac tgc att gat ttc agt tac ctg tta tat 336
 Met Lys Glu Asn Asp Thr His Cys Ile Asp Phe Ser Tyr Leu Leu Tyr
 100 105 110

agc cag aag ggg ttg aac cct ggc act ttg aat atc cta gtt agg gtg 384
 Ser Gln Lys Gly Leu Asn Pro Gly Thr Leu Asn Ile Leu Val Arg Val
 115 120 125

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Pro Ser Leu Pro Asp Tyr Glu Gly Val Asp Ala Ser Leu Asn Glu Thr	
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Lys Ser Asn Ala Ala Pro Gly Leu Leu Asn Val Tyr Val Lys Val Asn
 85 90 95

Asn Gly Pro Leu Gly Asn Pro Ile Trp Asn Ile Ser Gly Asp Pro Thr
 100 105 110

Arg Thr Trp His Arg Ala Glu Leu Ala Ile Ser Thr Phe Trp Pro Asn
 115 120 125

Phe Tyr Gln Val Ile Phe Glu Val Val Thr Ser Gly His Gln Gly Tyr
 130 135 140

Leu Ala Ile Asp Glu Val Lys Val Leu Gly His
 145 150 155

<210> 7
 <211> 154
 <212> PRT
 <213> Mus musculus

<400> 7
 Cys Lys Phe Gly Trp Gly Ser Gln Lys Thr Val Cys Asn Trp Gln His
 1 5 10 15

Asp Ile Ser Ser Asp Leu Lys Trp Ala Val Leu Asn Ser Lys Thr Gly
 20 25 30

Pro Val Gln Asp His Thr Gly Asp Gly Asn Phe Ile Tyr Ser Glu Ala
 35 40 45

Asp Glu Arg His Glu Gly Arg Ala Ala Arg Leu Met Ser Pro Val Val
 50 55 60

Ser Ser Ser Arg Ser Ala His Cys Leu Thr Phe Trp Tyr His Met Asp
 65 70 75 80

Gly Ser His Val Gly Thr Leu Ser Ile Lys Leu Lys Tyr Glu Met Glu
 85 90 95

Glu Asp Phe Asp Gln Thr Leu Trp Thr Val Ser Gly Asn Gln Gly Asp
 100 105 110

Gln Trp Lys Glu Ala Arg Val Val Leu His Lys Thr Met Lys Gln Tyr
 115 120 125

Gln Val Ile Val Glu Gly Thr Val Gly Lys Gly Ser Ala Gly Gly Ile
 130 135 140

Ala Val Asp Asp Ile Ile Ala Asn His
 145 150

<210> 8
 <211> 1452
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Arg Thr Leu Gly Thr Cys Leu Ala Thr Leu Ala Gly Leu Leu Leu
 1 5 10 15

Thr Ala Ala Gly Glu Thr Phe Ser Gly Gly Cys Leu Phe Asp Glu Pro
 20 25 30

Tyr Ser Thr Cys Gly Tyr Ser Gln Ser Glu Gly Asp Asp Phe Asn Trp
 35 40 45

Glu Gln Val Asn Thr Leu Thr Lys Pro Thr Ser Asp Pro Trp Met Pro
 50 55 60

Ser Gly Ser Leu Met Leu Val Asn Ala Ser Gly Arg Pro Glu Gly Gln
 65 70 75 80

Arg Ala His Leu Leu Leu Pro Gln Leu Lys Glu Asn Asp Thr His Cys
 85 90 95

Ile Asp Phe His Tyr Phe Val Ser Ser Lys Ser Asn Ser Pro Pro Gly
 100 105 110

Leu Leu Asn Val Tyr Val Lys Val Asn Asn Gly Pro Leu Gly Asn Pro
 115 120 125

Ile Trp Asn Ile Ser Gly Asp Pro Thr Arg Thr Trp Asn Arg Ala Glu
 130 135 140

Leu Ala Ile Ser Thr Phe Trp Pro Asn Phe Tyr Gln Val Ile Phe Glu
 145 150 155 160
 Val Ile Thr Ser Gly His Gln Gly Tyr Leu Ala Ile Asp Glu Val Lys
 165 170 175
 Val Leu Gly His Pro Cys Thr Arg Thr Pro His Phe Leu Arg Ile Gln
 180 185 190
 Asn Val Glu Val Asn Ala Gly Gln Phe Ala Thr Phe Gln Cys Ser Ala
 195 200 205
 Ile Gly Arg Thr Val Ala Gly Asp Arg Leu Trp Leu Gln Gly Ile Asp
 210 215 220
 Val Arg Asp Ala Pro Leu Lys Glu Ile Lys Val Thr Ser Ser Arg Arg
 225 230 235 240
 Phe Ile Ala Ser Phe Asn Val Val Asn Thr Thr Lys Arg Asp Ala Gly
 245 250 255
 Lys Tyr Arg Cys Met Ile Arg Thr Glu Gly Gly Val Gly Ile Ser Asn
 260 265 270
 Tyr Ala Glu Leu Val Val Lys Glu Pro Pro Val Pro Ile Ala Pro Pro
 275 280 285
 Gln Leu Ala Ser Val Gly Ala Thr Tyr Leu Trp Ile Gln Leu Asn Ala
 290 295 300
 Asn Ser Ile Asn Gly Asp Gly Pro Ile Val Ala Arg Glu Val Glu Tyr
 305 310 315 320
 Cys Thr Ala Ser Gly Ser Trp Asn Asp Arg Gln Pro Val Asp Ser Thr
 325 330 335
 Ser Tyr Lys Ile Gly His Leu Asp Pro Asp Thr Glu Tyr Glu Ile Ser
 340 345 350
 Val Leu Leu Thr Arg Pro Gly Glu Gly Thr Gly Ser Pro Gly Pro
 355 360 365
 Ala Leu Arg Thr Arg Thr Lys Cys Ala Asp Pro Met Arg Gly Pro Arg
 370 375 380
 Lys Leu Glu Val Val Glu Val Lys Ser Arg Gln Ile Thr Ile Arg Trp
 385 390 395 400
 Glu Pro Phe Gly Tyr Asn Val Thr Arg Cys His Ser Tyr Asn Leu Thr
 405 410 415
 Val His Tyr Cys Tyr Gln Val Gly Gly Gln Glu Gln Val Arg Glu Glu
 420 425 430
 Val Ser Trp Asp Thr Glu Asn Ser His Pro Gln His Thr Ile Thr Asn
 435 440 445

Leu Ser Pro Tyr Thr Asn Val Ser Val Lys Leu Ile Leu Met Asn Pro
 450 455 460
 Glu Gly Arg Lys Glu Ser Gln Glu Leu Thr Val Gln Thr Asp Glu Asp
 465 470 475 480
 Leu Pro Gly Ala Val Pro Thr Glu Ser Ile Gln Gly Ser Thr Phe Glu
 485 490 495
 Glu Lys Ile Phe Leu Gln Trp Arg Glu Pro Thr Gln Thr Tyr Gly Val
 500 505 510
 Ile Thr Leu Tyr Glu Ile Thr Tyr Lys Ala Val Ser Ser Phe Asp Pro
 515 520 525
 Glu Ile Asp Leu Ser Asn Gln Ser Gly Arg Val Ser Lys Leu Gly Asn
 530 535 540
 Glu Thr His Phe Leu Phe Gly Leu Tyr Pro Gly Thr Thr Tyr Ser
 545 550 555 560
 Phe Thr Ile Arg Ala Ser Thr Ala Lys Gly Phe Gly Pro Pro Ala Thr
 565 570 575
 Asn Gln Phe Thr Thr Lys Ile Ser Ala Pro Ser Met Pro Ala Tyr Glu
 580 585 590
 Leu Glu Thr Pro Leu Asn Gln Thr Asp Asn Thr Val Thr Val Met Leu
 595 600 605
 Lys Pro Ala Gln Ser Arg Gly Ala Pro Val Ser Val Tyr Gln Ile Val
 610 615 620
 Val Glu Glu Glu Arg Pro Arg Arg Thr Lys Lys Thr Thr Glu Ile Leu
 625 630 635 640
 Lys Cys Tyr Pro Val Pro Ile His Phe Gln Asn Ala Ser Leu Leu Asn
 645 650 655
 Ser Gln Tyr Tyr Phe Ala Ala Glu Phe Pro Ala Asp Ser Leu Gln Ala
 660 665 670
 Ala Gln Pro Phe Thr Ile Gly Asp Asn Lys Thr Tyr Asn Gly Tyr Trp
 675 680 685
 Asn Thr Pro Leu Leu Pro Tyr Lys Ser Tyr Arg Ile Tyr Phe Gln Ala
 690 695 700
 Ala Ser Arg Ala Asn Gly Glu Thr Lys Ile Asp Cys Val Gln Val Ala
 705 710 715 720
 Thr Lys Gly Ala Ala Thr Pro Lys Pro Val Pro Glu Pro Glu Lys Gln
 725 730 735
 Thr Asp His Thr Val Lys Ile Ala Gly Val Ile Ala Gly Ile Leu Leu
 740 745 750

Phe Val Ile Ile Phe Leu Gly Val Val Leu Val Met Lys Lys Arg Lys
 755 760 765
 Leu Ala Lys Lys Arg Lys Glu Thr Met Ser Ser Thr Arg Gln Glu Met
 770 775 780
 Thr Val Met Val Asn Ser Met Asp Lys Ser Tyr Ala Glu Gln Gly Thr
 785 790 795 800
 Asn Cys Asp Glu Ala Phe Ser Phe Met Asp Thr His Asn Leu Asn Gly
 805 810 815
 Arg Ser Val Ser Ser Pro Ser Ser Phe Thr Met Lys Thr Asn Thr Leu
 820 825 830
 Ser Thr Ser Val Pro Asn Ser Tyr Tyr Pro Asp Glu Thr His Thr Met
 835 840 845
 Ala Ser Asp Thr Ser Ser Leu Val Gln Ser His Thr Tyr Lys Lys Arg
 850 855 860
 Glu Pro Ala Asp Val Pro Tyr Gln Thr Gly Gln Leu His Pro Ala Ile
 865 870 875 880
 Arg Val Ala Asp Leu Leu Gln His Ile Thr Gln Met Lys Cys Ala Glu
 885 890 895
 Gly Tyr Gly Phe Lys Glu Glu Tyr Glu Ser Phe Phe Glu Gly Gln Ser
 900 905 910
 Ala Ser Trp Asp Val Ala Lys Lys Asp Gln Asn Arg Ala Lys Asn Arg
 915 920 925
 Tyr Gly Asn Ile Ile Ala Tyr Asp His Ser Arg Val Ile Leu Gln Pro
 930 935 940
 Val Glu Gly Asp Thr Asn Ser Asp Tyr Ile Asn Gly Asn Tyr Ile Asp
 945 950 955 960
 Gly Tyr His Arg Pro Asn His Tyr Ile Ala Thr Gln Gly Pro Met Gln
 965 970 975
 Glu Thr Ile Tyr Asp Phe Trp Arg Met Val Trp His Glu Asn Thr Ala
 980 985 990
 Ser Ile Ile Met Val Thr Asn Leu Val Glu Val Gly Arg Val Lys Cys
 995 1000 1005
 Cys Lys Tyr Trp Pro Asp Asp Thr Glu Ile Tyr Lys Asp Ile Lys Val
 1010 1015 1020
 Thr Leu Ile Glu Thr Glu Leu Leu Ala Glu Tyr Val Ile Arg Thr Phe
 1025 1030 1035 1040
 Ala Val Glu Lys Arg Gly Ile Ile Glu Ile Arg Glu Ile Arg Gln Phe
 1045 1050 1055

His Phe Thr Gly Trp Pro Asp His Gly Val Pro Tyr His Ala Thr Gly
 1060 1065 1070
 Leu Leu Gly Phe Val Arg Gln Val Lys Ser Lys Ser Pro Pro Ser Ala
 1075 1080 1085
 Gly Pro Leu Val Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Cys
 1090 1095 1100
 Phe Ile Val Ile Asp Ile Met Leu Asp Met Ala Glu Arg Glu Gly Val
 1105 1110 1115 1120
 Val Asp Ile Tyr Asn Cys Val Arg Glu Leu Arg Ser Arg Arg Val Asn
 1125 1130 1135
 Met Val Gln Thr Glu Glu Gln Tyr Val Phe Ile His Asp Ala Ile Leu
 1140 1145 1150
 Glu Ala Cys Leu Cys Gly Asp Thr Ser Val Pro Ala Ser Gln Val Arg
 1155 1160 1165
 Ser Leu Tyr Tyr Asp Met Asn Lys Leu Asp Pro Gln Thr Asn Ser Ser
 1170 1175 1180
 Gln Ile Lys Glu Glu Phe Arg Thr Leu Asn Met Val Thr Pro Thr Leu
 1185 1190 1195 1200
 Arg Val Glu Asp Cys Ser Ile Ala Leu Leu Pro Arg Asn His Glu Lys
 1205 1210 1215
 Asn Arg Cys Met Asp Ile Leu Pro Pro Asp Arg Cys Leu Pro Phe Leu
 1220 1225 1230
 Ile Thr Ile Asp Gly Glu Ser Ser Asn Tyr Ile Asn Ala Ala Leu Met
 1235 1240 1245
 Asp Ser Tyr Lys Gln Pro Ser Ala Phe Ile Val Thr Gln His Pro Leu
 1250 1255 1260
 Pro Asn Thr Val Lys Asp Phe Trp Arg Leu Val Leu Asp Tyr His Cys
 1265 1270 1275 1280
 Thr Ser Val Val Met Leu Asn Asp Val Asp Pro Ala Gln Leu Cys Pro
 1285 1290 1295
 Gln Tyr Trp Pro Glu Asn Gly Val His Arg His Gly Pro Ile Gln Val
 1300 1305 1310
 Glu Phe Val Ser Ala Asp Leu Glu Glu Asp Ile Ile Ser Arg Ile Phe
 1315 1320 1325
 Arg Ile Tyr Asn Ala Ala Arg Pro Gln Asp Gly Tyr Arg Met Val Gln
 1330 1335 1340
 Gln Phe Gln Phe Leu Gly Trp Pro Met Tyr Arg Asp Thr Pro Val Ser
 1345 1350 1355 1360

Lys Arg Ser Phe Leu Lys Leu Ile Arg Gln Val Asp Lys Trp Gln Glu
 1365 1370 1375

Glu Tyr Asn Gly Gly Glu Gly Pro Thr Val Val His Cys Leu Asn Gly
 1380 1385 1390

Gly Gly Arg Ser Gly Thr Phe Cys Ala Ile Ser Ile Val Cys Glu Met
 1395 1400 1405

Leu Arg His Gln Arg Thr Val Asp Val Phe His Ala Val Lys Thr Leu
 1410 1415 1420

Arg Asn Asn Lys Pro Asn Met Val Asp Leu Leu Asp Gln Tyr Lys Phe
 1425 1430 1435 1440

Cys Tyr Glu Val Ala Leu Glu Tyr Leu Asn Ser Gly
 1445 1450

<210> 9

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gagccgcggc tcgagttAAC cgccatggat gtggcggccg

40

<210> 10

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

gctcacagct agttcagccc

20

<210> 11

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 11

ctacacccac atctaacgaa ccgtgaagca ggg

33

<210> 12

<211> 4

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
cleavage motif

<400> 12
Arg Thr Lys Arg
1

<210> 13
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
modified cleavage motif

<400> 13
Leu Thr Asn Arg
1